

1638



RAW SEQUENCE LISTING PATENT APPLICATION: US/08/945,144

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DATE: 07/27/2000 TIME: 12:59:09

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3 <110> APPLICANT: Lebrun, Michel
              Sailland, Alain
              Freyssinet, Georges
      6 DeGryse, Eric
8 <120> TITLE OF INVENTION: Mutated 5-Enol Pyruvylshikimate-3-Phosphate Synthase,
              Gene Coding for Said Protein and Transformed Plants
              Containing Said Gene
     12 <130> FILE REFERENCE: 5500-13
     14 <140> CURRENT APPLICATION NUMBER: 08/945,144
C--> 15 <141> CURRENT FILING DATE: 1998-12-01
     17 <150> PRIOR APPLICATION NUMBER: PCT/FR96/01125
     18 <151> PRIOR FILING DATE: 1996-07-18
     20 <150> PRIOR APPLICATION NUMBER: FRANCE 95/08979
     21 <151> PRIOR FILING DATE: 1995-07-19
     23 <160> NUMBER OF SEQ ID NOS: 5
     25 <170> SOFTWARE: PatentIn Ver. 2.0
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     30 <213> ORGANISM: Zea mays
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     67 cgcgggagcc atttgggagg aaacacctca aggcgattga tgtcaacatg aacaagatgc 1080
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104
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                                                10
106 ggc acc gtc aag ctg ccg ggg tcc aag tcg ctt tcc aac cgg atc ctc
107 Gly Thr Val Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile Leu
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108
110 cta ctc gcc gcc ctg tcc gag ggg aca aca gtg gtt gat aac ctg ctg
111 Leu Leu Ala Ala Leu Ser Glu Gly Thr Thr Val Val Asp Asn Leu Leu
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                                        40
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114 aac agt gag gat gtc cac tac atg ctc ggg gcc ttg agg act ctt ggt 115 Asn Ser Glu Asp Val His Tyr Met Leu Gly Ala Leu Arg Thr Leu Gly
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119 Leu Ser Val Glu Ala Asp Lys Ala Ala Lys Arg Ala Val Val Gly 120 65 70 75
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123 Cys Gly Gly Lys Phe Pro Val Glu Asp Ala Lys Glu Glu Val Gln Leu
124 80 90 95
126 ttc ttg ggg aat gct gga act gca atg cgg cca ttg aca gca gct gtt 127 Phe Leu Gly Asn Ala Gly Thr Ala Met Arg Pro Leu Thr Ala Ala Val
                                                                              338
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128
                                                                  110
130 act gct gct ggt gga aat gca act tac gtg ctt gat gga gta cca aga
131 Thr Ala Ala Gly Gly Asn Ala Thr Tyr Val Leu Asp Gly Val Pro Arg
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                                    120
                                                             125
134 atg agg gag aga ccc att ggc gac ttg gtt gtc gga ttg aag cag ctt
135 Met Arg Glu Arg Pro Ile Gly Asp Leu Val Val Gly Leu Lys Gln Leu
          130
                                  135
138 ggt gca gat gtt gat tgt ttc ctt ggc act gac tgc cca cct gtt cgt 139 Gly Ala Asp Val Asp Cys Phe Leu Gly Thr Asp Cys Pro Pro Val Arg 140 145 \qquad 150 \qquad 155
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142 gtc aat gga atc gga ggg cta cct ggt ggc aag gtc aag ctg tct ggc 143 Val Asn Gly Ile Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser Gly 144 160 165 170 175
146 too atc agc agt cag tac ttg agt goc ttg ctg atg got got cct ttg
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151 Ala Leu Gly Asp Val Glu Ile Glu Ile Ile Asp Lys Leu Ile Ser Ile
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## AUG 0 8 2000

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155	152	000	+ 2.0	ata	195	2+4	303	++~	202	200	2+4	~ ~ ~	oat.	+++	205	a+a	222	671
156   210   215   220   225   220   3   3   3   3   3   3   3   3   3																		0/4
158   gca   gag   cat   tct   gat   agc   tgg   gac   aga   tct   tac   att   aag   gag   ggt   caa   722   159   Ala   Glu   His   Ser   Asp   Ser   Ttp   Asp   Arg   Phe   Tyr   Ile   Lys   Gly   Gly   Gly   Glo   Cas   Cas		FIU	ıyı		GIU	Met	1111	neu		пец	Met	Giu	ALG		GIĀ	Val	гуз	
159   Ala   Clu   His   Ser   Asp   Ser   Tip   Asp   Arg   Phe   Tyr   Tie   Lys   Gly   Gly   Gln		aca	αaα		tot	aat	anc	taa		ana	ttc	tac	att		aa a	aat	C22	722
160		-				-	-		-					-				122
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163   Lys   Tyr   Lys   Ser   Pro   Lys   Asn   Ala   Tyr   Val   Clu   Cly   Asp   Ala   Ser   Ser   164   240   245   250   250   250   255   255   255   266   266   266   266   267   267   267   270		aaa		ааσ	tee	cct	aaa		acc	tat	att	gaa		aat	acc	tca	age	770
164   240   245   250   255   3166   3ca   agc   agc																		,,,
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167 Åla Ser Tyr Phe Leu Åla Gly Åla Åla Ile Thr Gly Gly Thr Val Thr 260			age	tat	ttc	tta		aat	act	σса	att		ααa	aaa	act	ata		818
168																		0.10
171    Val   Glu   Gly   Cys   Gly   Thr   Thr   Ser   Leu   Gln   Gly   Asp   Val   Lys   Phe   Ala   280     174    gag   gta   ctg   gag   atg   atg   gga   gga   aag   gta   aca   tgg   acc   gag   act   agc   gga   gga   aag   gta   aca   tgg   acc   gag   act   agc   gag   aag   gta   aca   tgg   acc   gag   act   agc   gag   aag   act   acc   gag   agg   aag   act   acc   gag   aag   act   acc   gag   aag   act   acc   gag   aag   acc   acc   acc   gag   aag   acc				-1-				1					0-1	1				
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172																		
175   Glu   Val   Leu   Glu   Met   Met   Gly   Ala   Lys   Val   Thr   Trp   Thr   Glu   Thr   Ser   290   295   300   300   300   300   300   310   310   315												4						
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176																		
179    Val						•		-					-					
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183 Lys Ala Ile Asp Val Asn Met Asn Lys Met Pro Asp Val Ala Met Thr 184 320 325 330 335  186 ctt gct gtg gtt gcc ctc ttt gcc gat ggc ccg aca gcc atc aga gac 1058  187 Leu Ala Val Val Ala Leu Phe Ala Asp Gly Pro Thr Ala Ile Arg Asp 188 340 340 355 350  190 gtg gct tcc tgg aga gta aag gag acc gag agg atg gtt gcg atc cgg 1106  191 Val Ala Ser Trp Arg Val Lys Glu Thr Glu Arg Met Val Ala Ile Arg 192 355 350  194 acg gag cta acc aag ctg gga gca tct gtt gag gaa ggg ccg gac tac 1154  195 Thr Glu Leu Thr Lys Leu Gly Ala Ser Val Glu Gly Pro Asp Tyr 196 370 375  198 tgc atc acc acg ccg ccg gag aag ctg acg gtg acg gcg atc gac acg 1202  199 Cys Ile Ile Thr Pro Pro Glu Lys Leu Asn Val Thr Ala Ile Asp Thr 200 385 390 390  202 tac gac gac cac agg atg gcc atg gcc ttc tcc ctt gcc gcc gac acc 1202  203 Tyr Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala 204 400 400 405 405 410  206 gag gtc ccc gtc acc atc cgg gac cct ggc ccc gag ccc gag acc tcc gcc gag gcc ctc gac ccc gac acc ccc gac acc acc acc ac	180		305					310					315					
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188																		1058
190 gtg gct tcc tgg aga gta aag gag acc gag agg atg gtt gcg atc cgg   1106		Leu	Ala	Val	Val		Leu	Phe	Ala	Asp	_	Pro	Thr	Ala	Ile		Asp	
191																		
192																		1106
194 acg gag cta acc aag ctg gga gca tct gtt gag gaa ggg ccg gac tac 1154 195 Thr Glu Leu Thr Lys Leu Gly Ala Ser Val Glu Glu Gly Pro Asp Tyr 196 370 375 380  198 tgc atc atc acg ccg ccg gag aag ctg acg ggg ggg ggg gcg gcg gcg gcg gcg gc		Val	Ala	Ser		Arg	Val	Lys	Glu		Glu	Arg	Met	Val		Ile	Arg	
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203 Tyr Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala 400 415 410 415 416 415 416 415 416 416 415 416 416 416 416 416 416 416 416 416 416		tac		aac	cac	ann	atα		ato	acc	ttc	tec		acc	acc	t at	acc	1250
204 400 405 410 415 206 gag gtc ccc gtc acc atc cgg gac cct ggg tgc acc cgg aag acc ttc 1298 207 Glu Val Pro Val Thr Ile Arg Asp Pro Gly Cys Thr Arg Lys Thr Phe 420 430 210 ccc gac tac ttc gat gtg ctg agc act ttc gtc aag aat taa 1340 211 Pro Asp Tyr Phe Asp Val Leu Ser Thr Phe Val Lys Asn 212 435 440 215 <210> SEQ ID NO: 3 216 <211> LENGTH: 444																		1230
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309 <213> ORGANISM: Zea mays
311 <220> FEATURE:
312 <221> NAME/KEY: CDS
313 <222> LOCATION: (6)..(1337)
315 <400> SEQUENCE: 4
316 ccatg gcc ggc gcc gag gag atc gtg ctg cag ccc atc aag gag atc tcc 50
     Ala Gly Ala Glu Glu Ile Val Leu Gln Pro Ile Lys Glu Ile Ser
1 5 10 15
                                                   10
320 ggc acc gtc aag ctg ccg ggg tcc aag tcg ctt tcc aac cgg atc ctc
321 Gly Thr Val Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile Leu
                       20
322
                                                25
324 cta ctc gcc gcc ctg tcc gag ggg aca aca gtg gtt gat aac ctg ctg
325 Leu Leu Ala Ala Leu Ser Glu Gly Thr Thr Val Val Asp Asn Leu Leu 326 40 45
328 aac agt gag gat gtc cac tac atg ctc ggg gcc ttg agg act ctt ggt
329 Asn Ser Glu Asp Val His Tyr Met Leu Gly Ala Leu Arg Thr Leu Gly
330 50 60
330 50
332 ctc tct gtc gaa gcg gac aaa gct gcc aaa aga gct gta gtt gtt ggc
333 Leu Ser Val Glu Ala Asp Lys Ala Ala Lys Arg Ala Val Val Val Gly
334 65 70 75
336 tgt ggt gga aag ttc cca gtt gag gat gct aaa gag gaa gtg cag ctc 337 Cys Gly Gly Lys Phe Pro Val Glu Asp Ala Lys Glu Glu Val Gln Leu 338 80 85 90 95
340 ttc ttg ggg aat gct gga atc gca atg cgg tcc ttg aca gca gct gtt
                                                                                    338
341 Phe Leu Gly Asn Ala Gly Ile Ala Met Arg Ser Leu Thr Ala Ala Val
342
                    100
                                          105
344 act gct gct ggt gga aat gca act tac gtg ctt gat gga gta cca aga
345 Thr Ala Ala Gly Gly Asn Ala Thr Tyr Val Leu Asp Gly Val Pro Arg
346 115 120 125
348 atg agg gag aga ccc att ggc gac ttg gtt gtc gga ttg aag cag ctt
349 Met Arg Glu Arg Pro Ile Gly Asp Leu Val Val Gly Leu Lys Gln Leu
350 130 135 140
352 ggt gca gat gtt gat tgt ttc ctt ggc act gac tgc cca cct gtt cgt
353 Gly Ala Asp Val Asp Cys Phe Leu Gly Thr Asp Cys Pro Pro Val Arg 354 \phantom{-}145 \phantom{-}150 \phantom{-}155
356 gtc aat gga atc gga ggg cta cct ggt ggc aag gtc aag ctg tct ggc
                                                                                    530
357 Val Asn Gly Ile Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser Gly
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VERIFICATION SUMMARY
PATENT APPLICATION: US/08/945,144

DATE: 07/27/2000 TIME: 12:59:10

Input Set : A:\Rpmu5e.app
Output Set: N:\CRF3\07272000\H945144.raw

L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date